```
1   ATGAGCACGATTCCCAAACCTCAAAGAAAAACCAAACGTAACACCAAC
    MetSerThrIleProLysProGlnArgLysThrLysArgAsnThrAsn   16

49  CGTCGCCCACAGGACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGT
    ArgArgProGlnAspValLysPheProGlyGlyGlyGlnIleValGly   32

97  GGAGTTTACTTGTTGCCGCGCAGGGGCCCTAGATTGGGTGTGCGCGCG
    GlyValTyrLeuLeuProArgArgGlyProArgLeuGlyValArgAla   48

145 ACGAGGAAGACTTCCGAGCGGTCGCAACCTCGAGGTAGACGTCAGCCT
    ThrArgLysThrSerGluArgSerGlnProArgGlyArgArgGlnPro   64

193 ATCCCCAAGGCACGTCGGCCCGAGGGCAGGACCTGGGCTCAGCCCGGG
    IleProLysAlaArgArgProGluGlyArgThrTrpAlaGlnProGly   80

241 TACCCTTGGCCCCTCTATGGCAATGAGGGTTGCGGGTGGGCGGGATGG
    TyrProTrpProLeuTyrGlyAsnGluGlyCysGlyTrpAlaGlyTrp   96

289 CTCCTGTCTCCCCGTGGCTCTCGGCCTAGCTGGGGCCCCACAGACCCC
    LeuLeuSerProArgGlySerArgProSerTrpGlyProThrAspPro  112

337 CGGCGTAGGTCGCGCAATTTGGGTAAGGTCATCGATACCCTTACGTGC
    ArgArgArgSerArgAsnLeuGlyLysValIleAspThrLeuThrCys  128

385 GGCTTCGCGCACCTCATGGGGTACATACCGCTCGTCGGCGCCCCTCTT
    GlyPheAlaHisLeuMetGlyTyrIleProLeuValGlyAlaProLeu  144

433 GGAGGCCGTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGAC
    GlyGlyArgAlaArgAlaLeuAlaHisGlyValArgValLeuGluAsp  160

481 GGCGTGAACTATGCAACAGGGAACCTTCCTGGTTGCTCTTTCTCTATC
    GlyValAsnTyrAlaThrGlyAsnLeuProGlyCysSerPheSerIle  176

529 TTCCTTCTGGCCCTGCTCTCTTGCCTGACTGTGCCCGCTTCAGCCTAC
    PheLeuLeuAlaLeuLeuSerCysLeuThrValProAlaSerAlaTyr  192

577 CAAGTGCGCAATTCCTCAGGGCTTTACCAGGTCACCAATGATTGCCCT
    GlnValArgAsnSerSerGlyLeuTyrGlnValThrAsnAspCysPro  208

625 AATTCGAGTATTGTGTACGAGGCGGCCGATGCCATCCTGCACACTCCG
    AsnSerSerIleValTyrGluAlaAlaAspAlaIleLeuHisThrPro  224

673 GGGTGTGTCCCTTGCGTTCGCGAGGGTAACGCCTCGAGGTGTTGGGTG
    GlyCysValProCysValArgGluGlyAsnAlaSerArgCysTrpVal  240

721 GCGGTGACCCCCACGGTGGCCACCAGGGACGGCAAACTCCCCACAACG
    AlaValThrProThrValAlaThrArgAspGlyLysLeuProThrThr  256

769 CAGCTTCGACGTCATATCGATCTGCTTGTCGGGAGCGCCACCCTCTGC
    GlnLeuArgArgHisIleAspLeuLeuValGlySerAlaThrLeuCys  272
```

FIGURE 9

```
817  TCGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTCGTTGGT
     SerAlaLeuTyrValGlyAspLeuCysGlySerValPheLeuValGly  288

865  CAACTGTTTACCTTCTCTCCCAGGCGCCACTGGACGACGCAAGACTGC
     GlnLeuPheThrPheSerProArgArgHisTrpThrThrGlnAspCys  304

913  AATTGTTCTATCTATCCCGGCCATATAACGGGTCATCGCATGGCATGG
     AsnCysSerIleTyrProGlyHisIleThrGlyHisArgMetAlaTrp  320

961  GATATGATGATGAACTGG
     AspMetMetMetAsnTrp                                326
```

FIGURE 9 (CONT.)

```
1   ATGTCCCCTATACTAGGTTATTGGAAAATTAAGGGCCTTGTGCAACCC
    MetSerProIleLeuGlyTyrTrpLysIleLysGlyLeuValGlnPro   16

49  ACTCGACTTCTTTTGGAATATCTTGAAGAAAAATATGAAGAGCATTTG
    ThrArgLeuLeuLeuGluTyrLeuGluGluLysTyrGluGluHisLeu   32

97  TATGAGCGCGATGAAGGTGATAAATGGCGAAACAAAAAGTTTGAATTG
    TyrGluArgAspGluGlyAspLysTrpArgAsnLysLysPheGluLeu   48

145 GGTTTGGAGTTTCCCAATCTTCCTTATTATATTGATGGTGATGTTAAA
    GlyLeuGluPheProAsnLeuProTyrTyrIleAspGlyAspValLys   64

193 TTAACACAGTCTATGGCCATCATACGTTATATAGCTGACAAGCACAAC
    LeuThrGlnSerMetAlaIleIleArgTyrIleAlaAspLysHisAsn   80

241 ATGTTGGGTGGTTGTCCAAAAGAGCGTGCAGAGATTTCAATGCTTGAA
    MetLeuGlyGlyCysProLysGluArgAlaGluIleSerMetLeuGlu   96

289 GGAGCGGTTTTGGATATTAGATACGGTGTTTCGAGAATTGCATATAGT
    GlyAlaValLeuAspIleArgTyrGlyValSerArgIleAlaTyrSer  112

337 AAAGACTTTGAAACTCTCAAAGTTGATTTTCTTAGCAAGCTACCTGAA
    LysAspPheGluThrLeuLysValAspPheLeuSerLysLeuProGlu  128

385 ATGCTGAAAATGTTCGAAGATCGTTTATGTCATAAAACATATTTAAAT
    MetLeuLysMetPheGluAspArgLeuCysHisLysThrTyrLeuAsn  144

433 GGTGATCATGTAACCCATCCTGACTTCATGTTGTATGACGCTCTTGAT
    GlyAspHisValThrHisProAspPheMetLeuTyrAspAlaLeuAsp  160

481 GTTGTTTTATACATGGACCCAATGTGCCTGGATGCGTTCCCAAAATTA
    ValValLeuTyrMetAspProMetCysLeuAspAlaPheProLysLeu  176

529 GTTTGTTTTAAAAAACGTATTGAAGCTATCCCACAAATTGATAAGTAC
    ValCysPheLysLysArgIleGluAlaIleProGlnIleAspLysTyr  192

577 TTGAAATCCAGCAAGTATATAGCATGGCCTTTGCAGGGCTGGCAAGCC
    LeuLysSerSerLysTyrIleAlaTrpProLeuGlnGlyTrpGlnAla  208

625 ACGTTTGGTGGTGGCGACCATCCTCCAAAATCGGATCTGATCGAAGGT
    ThrPheGlyGlyGlyAspHisProProLysSerAspLeuIleGluGly  224

673 CGTGGGATCCCCAATTCGAGCTCGGTACCCATGAGCACGATTCCCAAA
    ArgGlyIleProAsnSerSerSerValProMetSerThrIleProLys  240

721 CCTCAAAGAAAAACCAAACGTAACACCAACCGTCGCCCACAGGACGTC
    ProGlnArgLysThrLysArgAsnThrAsnArgArgProGlnAspVal  256

769 AAGTTCCCGGGTGGCGGTCAGATCGTTGGTGGAGTTTACTTGTTGCCG
    LysPheProGlyGlyGlyGlnIleValGlyGlyValTyrLeuLeuPro  272
```

FIGURE 10

```
817  CGCAGGGGCCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAG
     ArgArgGlyProArgLeuGlyValArgAlaThrArgLysThrSerGlu  288

865  CGGTCGCAACCTCGAGGTAGACGTCAGCCTATCCCCAAGGCACGTCGG
     ArgSerGlnProArgGlyArgArgGlnProIleProLysAlaArgArg  304

913  CCCGAGGGCAGGACGGGGATCGGGAATTCATCGTGA
     ProGluGlyArgThrGlyIleGlyAsnSerSerEnd              315
```

FIGURE 10 (CONT.)